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SEARCHING GENE CENTERS OF THE GENUS CUCUMIS THROUGH HOST-PARASITE RELATIONSHIP[1]

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With 5 figures

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ABSTRACT

In addition to phytogeographic evidence, there are numerous host-specific pathogens, insects, and nematodes which point to Northeast Africa, Arabia and the eastern Mediterranean area as the possible primary gene center for the genus *Cucumis.* From this area the genus has radiated southward, eastward, and westward, forming secondary gene centers as indicated in the enclosed map. Cultivated cucumbers *(C. sativus)* are from India, but the origin of muskmelons (*C. melo)* is still uncertain. The West Indian gherkin *(C. anguria)* is believed to have been introduced into America from Africa at some past time.

INTRODUCTION

Considerable emphasis is now placed upon inherent resistance of vegetable cultivars to diseases, insects, and nematodes. Many breeding projects seek to combine resistance with other agronomic and horticultural characteristics for crop improvement. Explorers and collectors are searching for genuine sources of resistance among older cultivars and their wild ancestors. Detected genes for resistance frequently can be transferred to local cultivars or kept as inbred lines for further crossings and hybridization.

In common practice sources for resistance are sought from the assumed gene centers of cultivated plants, or from their wild progenitors, if known (17). In this paper a reverse method is proposed which attempts to locate the gene centers of cultivated crops according to their host-specific pests and pathogens. Recent investigations show that certain specialized parasites and their distribution on particular plant groups can serve as reliable indicators which help to trace back the origin and evolution of their hosts (16). Several reports listed here forecast the primary and secondary gene centers of the genus *Cucumis.*

MATERIALS AND METHOD

The New Crops Research Branch, Agricultural Research Service, U.S. Department of Agriculture maintains and propagates in its field stations some of the largest world collections of cultivated plants, as a gene bank for breeders and a reservoir of new characters for crop improvement. Plant introduction objectives and procedures in the United States are reported by HYLAND (14). Systematic screening of *Cucumis* intro-

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ductions from these collections have revealed a considerable number of genuine sources of resistance, collected from various exotic countries. Part of this work has been accomplished at the Regional Plant Introduction Stations, and part at the cooperative Experiment Stations of the Land Grant Colleges and Universities. Involved were diseases, insects, and nematodes as listed in Table 1. Detailed results of this screening are reported elsewhere (16).

TABLE 1. LIST OF DISEASES, INSECTS AND NEMATODES TESTED ON *Cucumis* SPP. NUMBERS AT RIGHT INDICATE THE TOTALS OF INTRODUCTIONS REPORTED RESISTANT.

A. DISEASES	Number of resistant introductions
Alternaria cucumerina (ELL. & EV.) ELLIOT, leaf blight (= *Macrosporium cucumerinum* ELL. & EV.)	10
Cladosporium cucumerinum ELL. & ARTH., scab	14
Colletotrichum lagenarium (PASS.) ELL. & HALST., anthracnose	17
Corynespora cassiicola (BERK. & CURT.) WEIR, leafspot	1
Corynespora melonis (COOKE) LINDAU, leafspot	1
Erwinia tracheiphila (E. F. SM.) HOLLAND, bacterial wilt	9
Erysiphe cichoracearum DC., powdery mildew	90
Mycosphaerella citrullina (C. O. SM.) GROSS., gummy stem blight	1
Pseudoperonospora cubensis (BERK. & CURT.) ROSTOW, downy mildew	34
Pseudomonas lachrymans (E. F. SM. & BRYAN) CARSNER, angular leafspot	14
Rhizoctonia spp., soil rot	1
Verticillium sp., wilt	4
unspecified disease resistance	6
B. VIRUS DISEASES	
Cucumber mosaic virus (CMV)	4
Mosaic	52
Squash mosaic virus (SMV)	1
Tobacco ring spot virus (TRSV)	16
Watermelon mosaic virus (WMV)	2
Viruses, not specified C T S	4
C. INSECTS	
Aphis spp., aphids	10
Acalymma vittata (F.), striped cucumber beetle	5
Diabrotica sp., cucumber beetle	4
Melon fly	1
Mites (*Bryobia* sp. and *Tetranychus*)	1
D. NEMATODES	
Meloidogyne incognita CHITW., cotton root-knot nematode	2

In screening this extensive material, the type of inheritance can be established, and the genes for resistance pinpointed in many cases, by using crosses and backcrosses of resistant introductions with some standard cultivars. Most of the introductions were tested only against one specific pathogen; some appeared to possess multiple resistance to several pests. More information, therefore, is needed to enhance the value of current breeding projects for crop improvement.

Evaluation of such screening results for the detection of primary and secondary gene centers of host plants follows.

SEARCHING GENE CENTERS OF *Cucumis*

It is not always easy for plant explorers to locate the primary and secondary gene centers for all the cultivated plants required in the further development of present civilization. For practical purposes, the classic textbooks of De CANDOLLE (1883) and VAVILOV (1949–1950) are still used with additional information published by ZHUKOVSKY (1959–1965), HARLAN (1961), HODGSON (1961), GORZ (1961), and others.

A new approach to the problem of origin and evolution of cultivated plants is now emerging within the scope of research activities of the New Crops Research Branch, Agricultural Research Service, U.S. Department of Agriculture. This is a synthesis of available phytogeographic data with the results of screening of introduced material. Pathological screening of this material enables one to establish sources of resistance and geographic areas of resistant hosts. Mapping of this information indicates the areas of greatest resistance and helps to locate gene centers for host plants (Fig. 5).

PHYTOGEOGRAPHIC EVIDENCE

The genus, *Cucumis* L. has about 30 species, distributed mostly in tropical East Africa, and the adjacent Arabian peninsula and eastern part of the Mediterranean area. This area has the greatest concentration of wild species that show phylogenetically older characteristics of the genus. This area also can be considered the primary gene center for *Cucumis* (see Fig. 5). Many good sources of disease resistance have been collected from this area. Wild species in the genus are predominantly annual or infrequently perennial herbs with climbing or prostrate stems and fleshy fruits; (cucumber is basically a berry with soft pericarp often called "pepo").

Three species in this genus are cultivated: the cucumber, *C. sativus* L., the muskmelon, *C. melo* L., and the gherkin, *C. anguria* L. In addition, the teasel gourd, *C. dipsaceus* EHRB., (Fig. 4) and the African horned cucumber, *C. metuliferus* E. MEY. (Fig. 3) are sporadically cultivated as ornamentals. *C. sativus* has 7 pairs of chromosomes, whereas the other species have 12.

Morphological characteristics of *Cucumis* and the geographical distribution of known species are described by COGNIAUX (1881, 1916), COGNIAUX and HARMS (1924), MÜLLER and PAX (1889) and others. Cultivated species *C. sativus* L. (cucumber), *C. melo* L. (muskmelon), and *C. anguria* L. (gherkin) are outlined by WHITAKER (1933, 1947), WHITAKER and DAVIS (1962), BOHN and WHITAKER (1965). The problem of the origin of the cultivated species is discussed by DE CANDOLLE (1883), VAVILOV (1949), MEEUSE (1958), WHYTE (1958), WEISS (1961) and ZHUKOVSKY (1964).

From the primary gene center the species of *Cucumis* have radiated in every direction and are now encountered in various geographic areas. Some members of this group moved southward into the vast grassland areas and savannas of South Africa. Here they form a secondary gene center with several prostrate species, such as *C. heptodactylus* NAUD. (Fig. 2), *C. leptodermis* SCHWEIK, *C. myriocarpus* NAUD. (Fig. 1) and others. These species show multiple resistance to several diseases and insects (LEPPIK 1966).

Another group moved eastward and formed a tertiary gene center in India, with *C. sativus* L., and *C. hardwickii* ROYLE as main representatives. In this gene center the cultivated cucumbers are believed to be indigenous. In India cucumbers have been cultivated for at least 3,000 years (De Candolle, 1883, Whitaker and Davis, 1962; Zhukovsky, 1964). They were introduced later into China and Europe.

Another gene center of *Cucumis* is in the West Indies with the half-cultivated, half-naturalized species *C. anguria* L. as a representative. The West Indian gherkin is believed to have been introduced into America from Africa by the slave trade. Meeuse (1958) found in Africa a wild species *C. longipes* Hook. f., which has many morphological characteristics in common with *C. anguria* L. These two species are cross-compatible, delivering highly fertile progeny in F_1 and F_2 generations. Meeuse concluded that the West Indian gherkin (*Cucumis anguria* L.) must be a cultigen descended from a non-bitter variant of the bitter-fruited African wild species, *C. longipes* Hook, f. Andrus, Bohn & Whitaker (1965) have partly repeated Meeuse's crossing experiments, with similar results.

Origin of muskmelons

The primary gene center of muskmelon, *Cucumis melo* L., is still unknown. Most authorities, including De Candolle (1883), Whitaker and Davis (1962, 1965), and Zhukovsky (1964), believe that this large polymorphous species is probably indigenous to tropical Africa. A number of observations indicate that muskmelon was introduced into Asia and Europe at a comparatively late date. There are well-developed, secondary gene centers of cultivated muskmelons in India, Persia, Iran, Southern Russia, and China (see 5–8 on map Fig. 5). The genes for resistance to powdery mildew have all occurred in collections from India according to Pryor, et al. (1964).

Pests, Pathogens, and Pollinators

The tropical nature of *Cucumis* is further evidenced by its special pests and pathogens. It is characteristic of this genus as of the whole family of Cucurbitaceae that no specialized rusts are found. Heteroecious rust families on higher angiosperms, such as Melampsoraceae, Gymnosporangiaceae, and Pucciniaceae, have all evolved in the northern hemisphere and only seldom have adapted themselves to live on genuine tropical plants. During a long cultivation of several cucurbits in the northern hemisphere, none of the numerous local rusts have yet settled on the cucumbers, although *Cucumis sativus* L. and *Bryonia dioica* Jacq. (a wild species in Europe), are susceptible by artificial inoculation to *Puccinia trabutii* Roum. & Sacc. (Gäumann, 1959, p. 753). A rare tropical rust *Uropyxis arisanensis* (Hirats, & Hash.) S. Ito & Murayama on *Melothria mucronata* Cogn., a tropical Cucurbitaceae, is reported by Hiratsuka and Hashioka (1941) from Formosa (Baxter, 1959: 224).

Further, the family Cucurbitaceae is, characteristically, either poorly represented or not represented at all, among butterfly (the Papilionoidea of the super family Lepidoptera) food plants. Ehrlich and Raven (1965) consider cucurbitacin a bitter-tasting terpene, repellant to several phytophagous insects and their larvae.

Contrary to the rust situation, powdery mildew caused by *Erysiphe cichoracearum* DC., has adapted to live on many Cucurbitaceae, including the genus *Cucumis*. Nevertheless, several wild cucumbers from India are immune to this pathogen, providing genuine sources of resistance for breeders. In addition, several wild species from Africa are resistant to powdery mildew, but they cannot be crossed easily with cultivated cucumbers.

In general, many wild species of *Cucumis* contain the genes for resistance to our common diseases and insects.

MAPPING THE WORLD DISTRIBUTION OF SOURCES OF RESISTANCE

For plant exploration purposes, a mapping of areas which have yielded the highest number of resistant species and varieties is desirable. Such maps help explorers and collectors to concentrate their efforts on areas of greatest variability of agricultural characteristics and pest resistance.

Fig. 5 shows the geographic distribution of sources of resistance, as documented in the above-mentioned reports. Black dots indicate the place where resistant introductions have been collected. In many cases, however, only the country of origin is known.

Encircled areas are the presumed primary and secondary gene centers of the genus *Cucumis*. No. 1 is the supposed primary center of the distribution of wild cucumbers. This area contains the largest number of resistant species and varieties; many of them possess multiple resistance.

No. 2 represents an ecological group of grassland species that may have been derived from the first group. These species are highly resistant to several of our diseases and insects. Multiple resistance is common in these species.

No. 3 is the supposed secondary gene center of the gunus *Cucumis*, represented by *Cucumis sativus* L. and closely related wild form *C. hardwickii* ROYLE. A number of good breeding stocks have come from this area.

No. 4 is the West Indian area of *C. anguria* L. which is presumably a domesticated form of the African wild species, *C. longipes* HOOK. f., as proved cytogenetically by MEEUSE (1958).

Nos. 5 to 8 are the assumed secondary gene centers for cultivated muskmelons, *C. melo* L., in India, China, Iran (Persia), and southern Russia.

Black arrows on the enclosed map indicate the supposed direction of distribution of the sections from the main gene-center of the genus Cucumis in Northeast Africa. Encircled numbers: (n–7) and (n–12) indicate the pairs of chromosomes in species.

This preliminary sketch of available data and information does not pretend to be complete or final. Its only purpose is to indicate the apparent correlation between the distribution of known sources of resistance and the presumed gene-centers of host plants according to VAVILOV, COGNIAUX; HARMS, MEEUSE, and others. Further investigation and exploration probably will provide more data and information about these areas. Of course the map will be altered accordingly.

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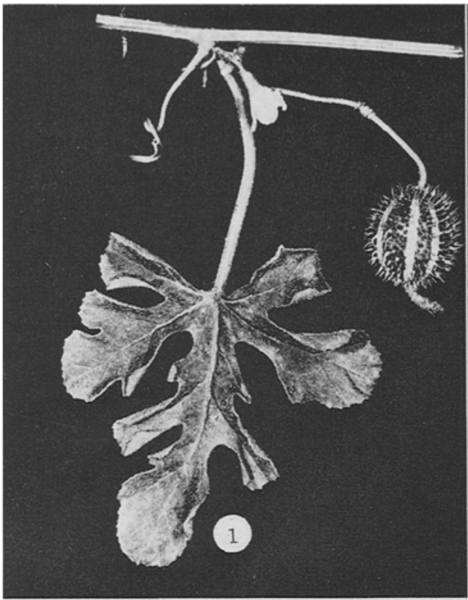

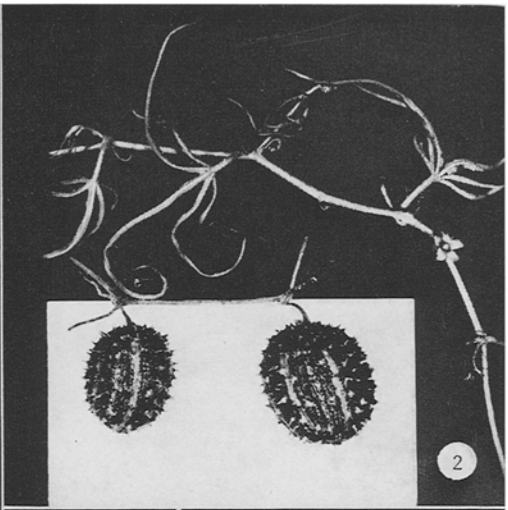

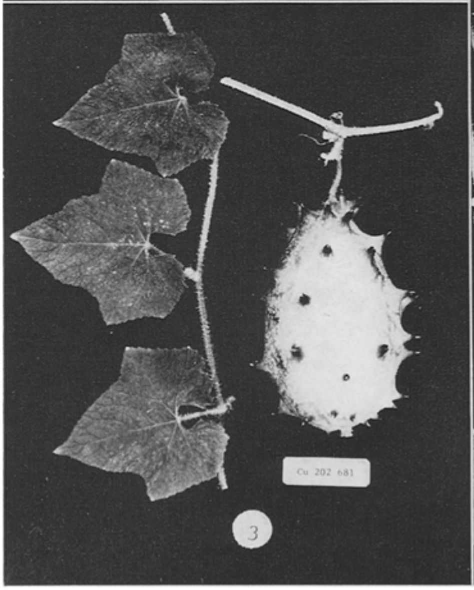

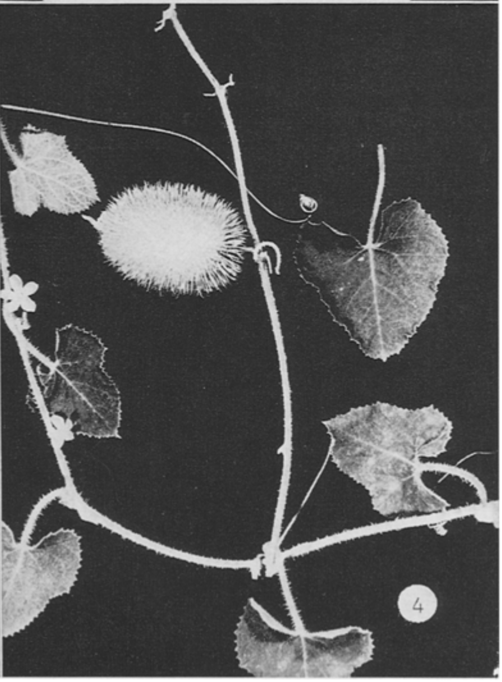

FIG. 1. *Cucumis myriocarpus* NAUD., native to South Africa. Leaf, flower and fruit. Shows multiple resistance.

FIG. 2. *C. heptodactylus* NAUD., native to South Africa. Note unique narrow leaves and small round fruits.

FIG. 3. *C. metuliferus* E. MEYER, from South Africa, resistant to powdery mildew and aphids.

FIG. 4. *C. dipsaceus* EHRENB., from Ethiopia. Flowers, leaves and fruits.

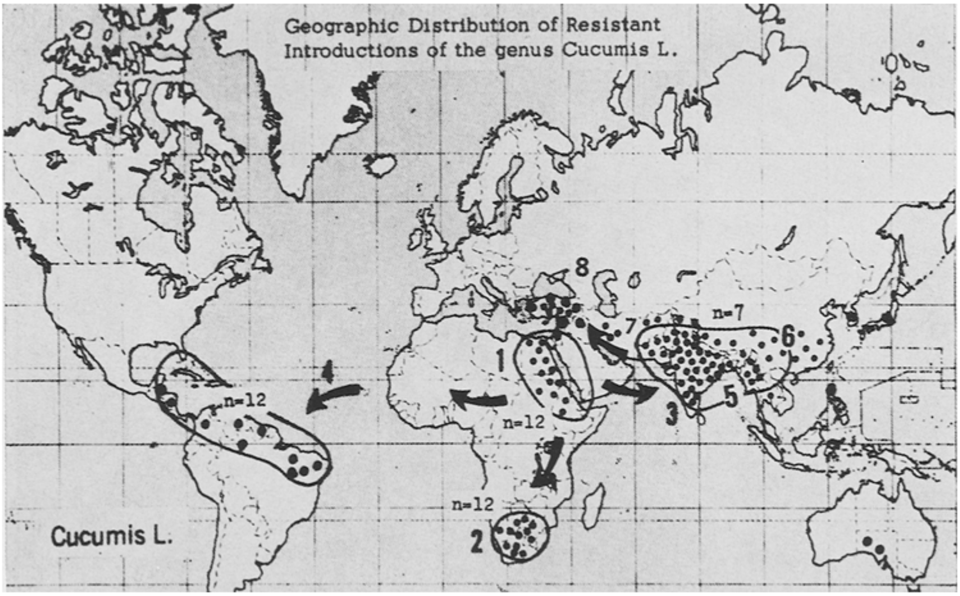

FIG. 5. Geographic distribution of resistant introductions of the genus *Cucumis* L. (black dots) Encircled areas indicate gene centers (1–8), n = number of chromosomes.